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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/970,820

DATE: 02/27/2002
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Input Set : A:\785332aa.app
Output Set: N:\CRF3\02272002\I970820.raw

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SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: FALB, DEAN A.
8 (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
9 TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
11 (iii) NUMBER OF SEQUENCES: 38
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: PENNIE & EDMONDS
15 (B) STREET: 1155 Avenue of the Americas
16 (C) CITY: New York
17 (D) STATE: New York
18 (E) COUNTRY: USA
19 (F) ZIP: 10036-2711
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/970,820
C--> 29 (B) FILING DATE: 05-Oct-2001
30 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US 08/386,844
34 (B) FILING DATE: 10-FEB-1995
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Coruzzi, Laura A.
38 (B) REGISTRATION NUMBER: 30,742
39 (C) REFERENCE/DOCKET NUMBER: 7853-032
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (212) 790-9090
43 (B) TELEFAX: (212) 869-8864
44 (C) TELEX: 66141 PENNIE
47 (2) INFORMATION FOR SEQ ID NO: 1:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 288 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: both
53 (D) TOPOLOGY: unknown
55 (ii) MOLECULE TYPE: cDNA
57 (iii) HYPOTHETICAL: NO
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 GGCITAGATG CAGCCTGCAA ATTAAACITT GATTTTTCAT CTIGTGAAAG CAGTCCTTGT 60

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66 TCCTATGGCC TAATGAACAA CTTCAGGTA ATGAGTAIGG TGTGAGGATT TACACCACIA      120
68 ATTTCIGCAG GTATATTTTC AGCCACICTT TCITCAGCAT TAGCATCCCT AGTGAGTGCT      180
70 CCCCCAAATAT TTCAGGCTCT ATGTAAGGAC AACATCTACC CAGCTTTCCA GATGTTTGCT      240
72 AAAGGTTATG GGAAAAATAA TGAACCTCTT CGTGGCTGCA TCTAAGCC      288
74 (2) INFORMATION FOR SEQ ID NO: 2:
76     (i) SEQUENCE CHARACTERISTICS:
77         (A) LENGTH: 178 base pairs
78         (B) TYPE: nucleic acid
79         (C) STRANDEDNESS: both
80         (D) TOPOLOGY: unknown
82     (ii) MOLECULE TYPE: cDNA
84     (iii) HYPOTHETICAL: NO
89     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
91 AAAAATAAAT AAATTAAAGT CTGAGACCAA TTGCCACTG TGAATATAAG CACATTAACC      60
93 CCAGGAGGAG CCAAGAACTA CACAAACCTC TCTATGAGAA TTTACCAGTC TTCTTTCATT      120
95 TGGCAAGAAA AAGCTCAGGA AAATTTGCTT GTTTAAATTC TATGAGCCTA GTCTATGG      178
97 (2) INFORMATION FOR SEQ ID NO: 3:
99     (i) SEQUENCE CHARACTERISTICS:
100         (A) LENGTH: 101 base pairs
101         (B) TYPE: nucleic acid
102         (C) STRANDEDNESS: both
103         (D) TOPOLOGY: unknown
105     (ii) MOLECULE TYPE: cDNA
107     (iii) HYPOTHETICAL: NO
112     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
114 GGGTAATTCA TTAATTACAC TTAAAATTG GAAAGTGGGA TAAGAAATCT AAAGTAAACC      60
116 AGCTTATCTT TGAAACAATA TTATTTTGAA ATTGGCTTTA A      101
118 (2) INFORMATION FOR SEQ ID NO: 4:
120     (i) SEQUENCE CHARACTERISTICS:
121         (A) LENGTH: 184 base pairs
122         (B) TYPE: nucleic acid
123         (C) STRANDEDNESS: both
124         (D) TOPOLOGY: unknown
126     (ii) MOLECULE TYPE: cDNA
128     (iii) HYPOTHETICAL: NO
133     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
135 GGCTTGGTGG TGATGCCTAC AAGAAATGTT TACATACAAA CACTCTATAC ATCTAACTCC      60
137 CGAAAAAGGA CCAGCTATTT CGGCAACAGA AAAAAGACAA GCATTTTCTAGA GGAGCGTTGC      120
139 TTTCTTAA GACCTAACTC ACTTAAGTCT TACAAACAGA AATAACAAGG AGGACAATTT      180
141 TCTA      184
143 (2) INFORMATION FOR SEQ ID NO: 5:
145     (i) SEQUENCE CHARACTERISTICS:
146         (A) LENGTH: 284 base pairs
147         (B) TYPE: nucleic acid
148         (C) STRANDEDNESS: both
149         (D) TOPOLOGY: unknown
151     (ii) MOLECULE TYPE: cDNA
153     (iii) HYPOTHETICAL: NO
158     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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160 CTIGGGGATG CTGTTTGGAG GAATCCTCAT GAAGCGCTTT GTTTTCTCTC TACAAGCCAT      60
162 TCCCCGCATA GCTACCACCA ICATCACCAT CTCATGATC CTTTGTGTTC CTTTGTTCCT      120
164 CATGGGATGC TCCACCCCAA CTGTGGCCGA AGTCTACCCC CCTAGCACAT CAAGTTCTAT      180
166 ACATCCGCAG TCTCCTGCCT GCCGCAGGGA CTGCTCGTGC CCAGATTCTA TCTTCCACCC      240
168 GGTCTGTGGA GACAAATGGAA TCGAGTACCT CTCCTCTTGC CATG      284
170 (2) INFORMATION FOR SEQ ID NO: 6:
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 2582 base pairs
174 (B) TYPE: nucleic acid
175 (C) STRANDEDNESS: both
176 (D) TOPOLOGY: unknown
178 (ii) MOLECULE TYPE: cDNA
180 (iii) HYPOTHETICAL: NO
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
187 GGCTTACCAT CGATGCGGCC GCGGATCCAG GGCTCAGAGG GAGGACGCAC CCGCCAGCCA      60
189 GCGGGGAACC TTCCCTCGCG GGCTCCCAGG GCGGTCTCTT TCCTCTCTCT AGCCCTGCTC      120
191 AGGCATTCCG CAGGTCCAGC AGAGGTACAC CTCCTGCAGC GGGTTCCAAAG TGCACCTCCA      180
193 GCGTGATGGA CCTGACCAAG GAGGCTTCCA GGAGCACAGA AGGGGCTGCA ACCCAGGTAC      240
195 CCAGAGAGTG AGCAGCTCCA CGCGGGACTG TGCACGGTGG CCGACACCCG CAGGGACGCC      300
197 CACCGGACGA GCACGCGGAG GGCCCTCGCC TCCACGGATG CACCATGCCG GTGTGAGGAG      360
199 CATCTGTTCT TCCACTCTC TGCAGTTAAC AAACCCAACC CAAACCAACA CAGGTGCTCC      420
201 TCCTGGGGAG TTTCTGTCT GACAAATGCC AGGCTCACTT CAAGGAGAAT CACGCTTCTT      480
203 TCTAAAGATG GATTACCAT TTAACAACA GCTCTGGGAG CCTTTCGGCA AATCTTGAAA      540
205 GCTGCACGGC GCAGAGACAT GGATGTGACT TCCCAAGCCC GGGGCGTAGG CCGTGAGATG      600
207 TACCCAGGCA CCGCGCAGCC TCGGGCCCCC AACACCACCT CCCCCGAGCT CAACCTGTCC      660
209 CACCCGCTCC TGGGCACCGC CCTGGCCAAT GGGACAGGTG AGCTCTCGGA GCACCAGCAA      720
211 TACGTGATCG GCCTGTTTCT CTCGTGCCCT TACACCATCT TCCTCTTCCC CATCGGCTTT      780
213 GTGGGCAACA TCCTGATCCT GGTGGTGAAC ATCAGCTTCC GCGAGAAGAT GACCATCCCC      840
215 GACCTGTACT TCATCAACCT GCGGTGCGC GACCTCATCC TGGTGGCCGA CTCCTCATTT      900
217 GAGGTGTTCA ACCTGCACGA GCGGTACTAC GACATCGCCG TCCTGTGCAC CTTTATGTCC      960
219 CTCCTCCTGC GGGTCAACAT GTACAGCAGC GTCTTCTTCC TCACCTGGAT GAGCTTCGAC      1020
221 CGCTACATCG CCCTGGCCAG GGCCATGCGC TGCAGCCTGT TCCGCACCAA GCACCACGCC      1080
223 CCGCTGAGCT GTGGCCTCAT CTGGATGGCA TCCGTGTCAG CCACGCTGGT GCCCTTACCC      1140
225 GCGGTGCACC TGCAGCACAC CGACGAGGCC TGCTTCTGTT TCGCGGATGT CCGGGAGGTG      1200
227 CAGTGGCTCG AGGTCACGCT GGGCTTCATC GTGCCCTTCG CCATCATCGG CCTGTGCTAC      1260
229 TCCCTCATTG TCCGGGTGET GGTGAGGCG CACCGGCACC GTGGGCTGCG GCGGCGCGG      1320
231 CAGAAGCGC TCCGCATGAT CCTCGCAGTG GTGCTGGTCT TCTTCGTCTG CTGGCTGCCG      1380
233 GAGAACGTCT TCATCAGCGT GCACCTCCTG CAGCGGACGC AGCCTGGGGC CGCTCCTTGC      1440
235 AAGCAGTCTT TCCGCCATGC CCACCCCTC ACGGGCCACA TTGTCAACCT CGCCGCTTTC      1500
237 TCCAACAGCT GCCTAAACCC CCTCATCTAC AGCTTTCTCG GGGAGACCTT CAGGGACAAG      1560
239 CTGAGGCTGT ACATTGAGCA GAAAACAAAT TTGCCGGCCC TGGACCGCTT CTGTACGCT      1620
241 GCCCTGAAGG CCGTCATTCC AGACAGCACC GAGCAGTCGG ATGTGAGGTT CAGCAGTGCC      1680
243 GTGTAGACAG CCTTGGCCGC ATAGGCCAG CCAGGTGTG ACTCGGGAGC TGCACACACC      1740
245 TGGGTGGACA CAAGGCACGG CCACGTCATG TCTCTAAACT GCGGTCAGAT GTGGCTTCTG      1800
247 GCTCCTCGGG CCTCGCGAGG GTCACGCTTG CCTGGTCAAC CTGGGGCTGC TTAGGAAACC      1860
249 TCAGGACTGG TCACCTTGCA CTCCTCACAC AGAATTGCTA CAATCCCAAA GCGCTCGCCC      1920
251 CGCAGGTGCC AAAGGCCAGC GGTGACCAGC CTGTACCCCA GCTCCTCCCC GCGAACCTTG      1980
253 CTGCGCGCTG CACCTGCCCG CTGCTGCAGG AAACATTTCT GACACCGTCG ACCAGGAAAG      2040
255 CCACACGGAG AGGCCACTGT GGGTGAAGCG CCTCAGTTAC ACAGGAACCC TAAAGCAAAT      2100

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257 CIGCCACCGT GGGGGAACIG ACGCTGGAGA IGCAAGGTGC TGGTGGGTCT GAGCTGGACG      2160
259 TCGCGGTGTG TCCTCTGTGC CCACGGTCTG AGCTAGCTAG CGCACCGCCG AGTTAAAGAG      2220
261 GAGAAGGAAA ACATGCTGCT CTGGTGCACG CCTGAGCGTC CTCATCTTC CAGGATGGCA      2280
263 GCAATGGCGC TGTGCGGCCT CACCAGGCCG ACGAGGAGCA GCAGCGCTCG GCCCGGAGCA      2340
265 GCAGGAAGGC CCCTCTGTGG AGCGCCCGCC GTCTGCTCCG GGGTGGTTCA GTCACGTCTT      2400
267 GTTGACATCA ACATGGCAAT TGCATCATG TGGACTGGGA CCGTGCAGAG TGCCGTGTGG      2460
269 GTTAGTCGGG TGCCAGGACA ATGAAATACT CCAGCACCTG TGGCTGACGA ATTCGTTTCT      2520
271 ACAGAAGTAA CAGCTGGGGA CAACTGCGAT GATGATGTAA AAACCTTCCC ATAAAATAAG      2580
273 CC                                                                                   2582

275 (2) INFORMATION FOR SEQ ID NO: 7:
277     (i) SEQUENCE CHARACTERISTICS:
278         (A) LENGTH: 128 base pairs
279         (B) TYPE: nucleic acid
280         (C) STRANDEDNESS: both
281         (D) TOPOLOGY: unknown
283     (ii) MOLECULE TYPE: cDNA
285     (iii) HYPOTHETICAL: NO
290     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
292 GGGAGGTGGG CTCCTGCTCA TCCTAGGCAT CGCACTGATT GTTACCTGTT GCAGAAAGAA      60
294 TAAAAATGAC ATAAGCAAAC TCATCTTCAA AAGTGGAGAT TTCCAAATGT CCCCCTATGC      120
296 TGAATACC                                                                                   128

298 (2) INFORMATION FOR SEQ ID NO: 8:
300     (i) SEQUENCE CHARACTERISTICS:
301         (A) LENGTH: 13 base pairs
302         (B) TYPE: nucleic acid
303         (C) STRANDEDNESS: single
304         (D) TOPOLOGY: linear
306     (ii) MOLECULE TYPE: DNA (genomic)
308     (iii) HYPOTHETICAL: NO
311     (ix) FEATURE:
312         (A) NAME/KEY: misc_feature
313         (B) LOCATION: 12
316     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
318 TTTTTTTTTT TNG                                                                                   13

320 (2) INFORMATION FOR SEQ ID NO: 9:
322     (i) SEQUENCE CHARACTERISTICS:
323         (A) LENGTH: 10 base pairs
324         (B) TYPE: nucleic acid
325         (C) STRANDEDNESS: single
326         (D) TOPOLOGY: linear
328     (ii) MOLECULE TYPE: DNA (genomic)
330     (iii) HYPOTHETICAL: NO
335     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
337 AGCATGGCTC                                                                                   10

339 (2) INFORMATION FOR SEQ ID NO: 10:
341     (i) SEQUENCE CHARACTERISTICS:
342         (A) LENGTH: 23 base pairs
343         (B) TYPE: nucleic acid
344         (C) STRANDEDNESS: single

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345         (D) TOPOLOGY: linear
347     (ii) MOLECULE TYPE: DNA (genomic)
349     (iii) HYPOTHETICAL: NO
354     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
356 CACCCCTGGC ATCTICCT TCC                                     23
358 (2) INFORMATION FOR SEQ ID NO: 11:
360     (i) SEQUENCE CHARACTERISTICS:
361         (A) LENGTH: 24 base pairs
362         (B) TYPE: nucleic acid
363         (C) STRANDEDNESS: single
364         (D) TOPOLOGY: linear
366     (ii) MOLECULE TYPE: DNA (genomic)
368     (iii) HYPOTHETICAL: NO
373     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
375 ATCTCCCCC AGTTCACCCC ATCC                                     24
377 (2) INFORMATION FOR SEQ ID NO: 12:
379     (i) SEQUENCE CHARACTERISTICS:
380         (A) LENGTH: 21 base pairs
381         (B) TYPE: nucleic acid
382         (C) STRANDEDNESS: single
383         (D) TOPOLOGY: linear
385     (ii) MOLECULE TYPE: DNA (genomic)
387     (iii) HYPOTHETICAL: NO
392     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
394 CCTGATAGAT GGGCACTGTG T                                     21
396 (2) INFORMATION FOR SEQ ID NO: 13:
398     (i) SEQUENCE CHARACTERISTICS:
399         (A) LENGTH: 22 base pairs
400         (B) TYPE: nucleic acid
401         (C) STRANDEDNESS: single
402         (D) TOPOLOGY: linear
404     (ii) MOLECULE TYPE: DNA (genomic)
406     (iii) HYPOTHETICAL: NO
411     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
413 GAACACGGCA TTGTCACTAA CT                                     22
415 (2) INFORMATION FOR SEQ ID NO: 14:
417     (i) SEQUENCE CHARACTERISTICS:
418         (A) LENGTH: 22 base pairs
419         (B) TYPE: nucleic acid
420         (C) STRANDEDNESS: single
421         (D) TOPOLOGY: linear
423     (ii) MOLECULE TYPE: DNA (genomic)
425     (iii) HYPOTHETICAL: NO
430     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
432 AAGTCGCGCC CGCCCCTGAA AT                                     22
434 (2) INFORMATION FOR SEQ ID NO: 15:
436     (i) SEQUENCE CHARACTERISTICS:
437         (A) LENGTH: 24 base pairs
438         (B) TYPE: nucleic acid

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format. [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format. [(B) FILING DATE:]